

Fig. 1A

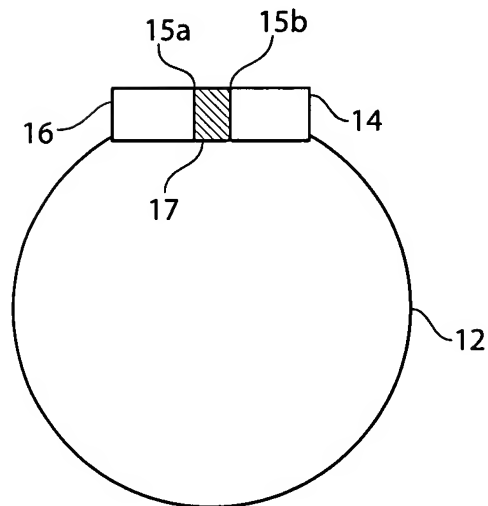


Fig. 1B

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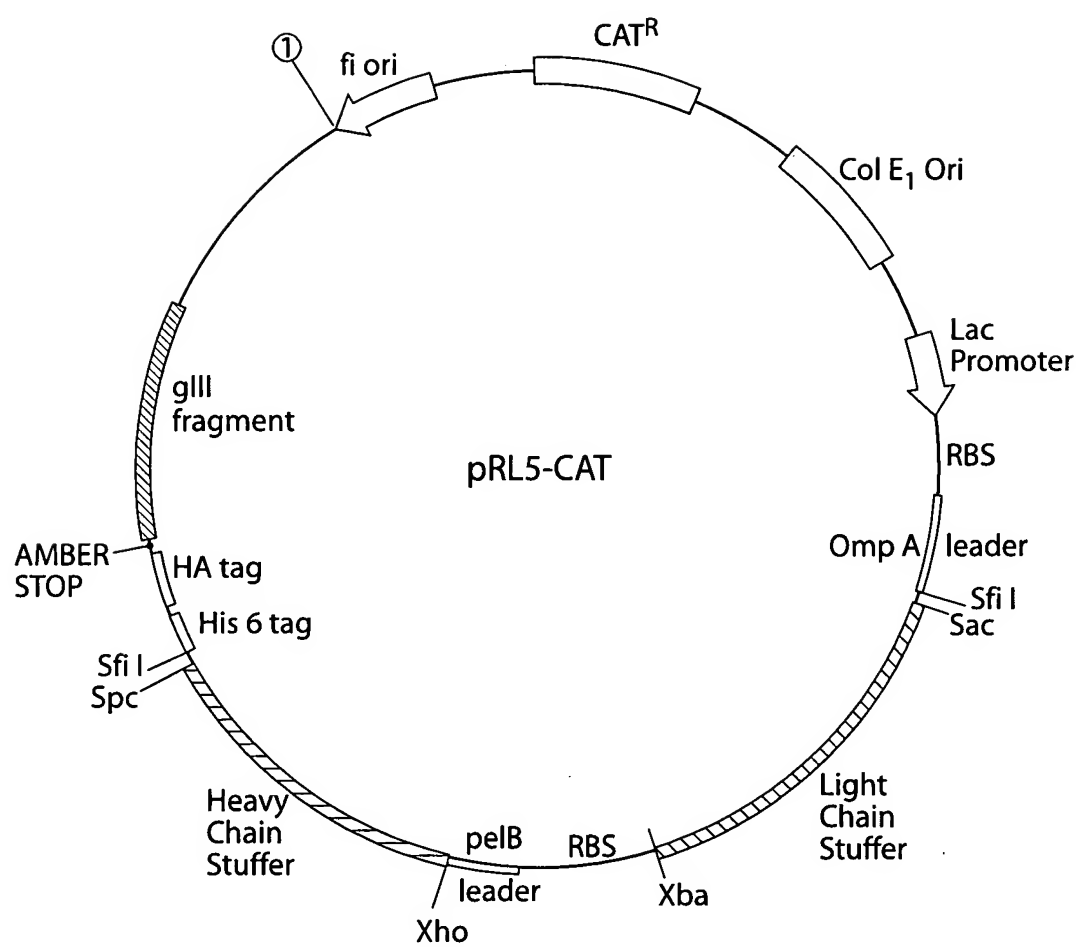


Fig. 2

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**PRL5-CAT**

5' GGGAAATTGTAAGCGTTAATATTTTGTAAATTCGCGTTAAATTTTGTTA  
AATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAAT  
CAAAAGAATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTGAACAAGAG  
TCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTAT  
CAGGGCGATGGCCCACTACGTGAACCATCACCTAATCAAGTTTTTTGGGGTC  
GAGGTGCCGTAAAGCACTAAATCGGAACCTAAAGGGAGCCCCGATTTAGA  
GCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGC  
GAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACCGCTGCGCGT  
AACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGC  
ACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTCTAAATACA  
TTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAAT  
ATTGAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCC  
TTTTTTGCGGCATTTTGCCCTTCTGTTTTGTCTACCCAGAAACGCTGGTGAAA  
GTAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTACATCGAACTGG  
ATCTCAACAGCGGTAAGATCCTTGAGAGTTTTTCGCCCCGAAGAACGTTTTCCA  
ATGATGAGCACTTTTCGACCGAATAAATACCTGTGACGGAAGATCACTTCGC  
AGAATAAATAAATCCTGGTGTCCCTGTTGATACCGGGAAGCCCTGGGCCAAC  
TTTTTGCGGAAAATGAGACGTTGATCGGCACGTAAGAGGTTCCAACTTTCACC  
ATAATGAAAATAAGATCACTACCGGGCGTATTTTTTTGAGTTGTGAGATTTTCA  
GGAGCTAAGGAAGCTAAAATGGAGAAAAAAATCACTGGATATAACCACCGTT  
GATATATCCCAATGGCATCGTAAAGAACATTTTGAGGCATTTTCAGTCAGTTGC  
TCAATGTACCTATAACCAGACCGTTTCAGCTGGATATTACGGCCTTTTTAAAGA  
CCGTAAAGAAAAATAAGCACAGTTTTATCCGGCCTTTATTTCACATTCTTGCC  
CGCTGATGAATGCTCATCCGGAATTACGTATGGCAATGAAAGACGGTGAGC  
TGGTGATATGGGATAGTGTTACCCCTTGTTACACCGTTTTCCATGAGCAAAC  
GAAACGTTTTTCATCGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCT  
ACACATATATTGCAAGATGTGGCGTGTTACGGTGAAAACCTGGCCTATTTCC  
CTAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGT  
TTCACCAGTTTTTGATTTAAACGTGGCCAATATGGACAACTTCTTCGCCCCCGT  
TTTCACCATGGGCAAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTG  
GCGATTTCAGGTTTCATCATGCCGTTTGTGATGGCTTCATGTGCGCAGAATGCT  
TAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCGTAATTTTTT  
TAAGGCAGTTATTGGTGCCCTTAAACGCCTGGTTGCTACGCCTGAATAAGTGA  
TAATAAGCGGATGAATGGCAGAAATTCGAAAGCAAATTCGACCCGGTCGTCG  
GTTTCAGGGCAGGGTCGTAAATAGCCGCTTATGTCTATTGCTGGTTTACCGGT  
TTATTGACTACCGGAAGCAGTGTGACCGTGTGCTTCTCAAATGCCTGAGGCCA  
GTTTGCTCAGGCTCTCCCCGTGGAGGTAATAATTGACGATATGATCCTTTTTT  
TCTGATCAAAAAGGATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAA  
ATCCCTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGAT  
CAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAA  
CAAAAAACCACCGCTACCAGCGGTGGTTTGTGTTGCCGGATCAAGAGCTACC  
AACTCTTTTTCCGAAGGTAACCTGGCTTCAGCAGAGCGCAGATACCAAATACT  
GTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACC  
GCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCG

Fig. 3A

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ATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGC  
GCAGCGGTGCGGCTGAACGGGGGGTTCGTGCACACAGCCAGCTTGGAGCGA  
ACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCA  
CGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTGC  
GAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTT  
ATAGTCCTGTGCGGTTTTGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGC  
TCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTAC  
GGTTCCTGGCCTTTTTGCTGGCCTTTTTGCTCACATGTTCTTTCCTGCGTATCCC  
CTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGC  
CGCAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAG  
CGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCA  
GCTGGCACGACAGGTTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAAT  
TAATGTGAGTTAGCTCACTCATTAGGCACCCAGGCTTTACACTTTATGCTTC  
CGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTGAATTCAGGAGG  
AATTTAAAATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTGGTTT  
CGCTACCGTGGCCCAGGCGGCCGAGCTCGACTGCACTGGATGGTGGCGCTGG  
ATGGTAAGCCGCTGGCAAGCGGTGAAGTGCCTCTGGATGTCGCTCCACAAGG  
TAAACAGTTGATTGAACTGCCTGAACTACCGCAGCCGGAGAGCGCCGGGCAA  
CTCTGGCTCACAGTACGCGTAGTGCAACCGAACGCGACCGCATGGTCAGAAG  
CCGGGCACATCAGCGCCTGGCAGCAGTGGCGTCTGGCGGAAAACCTCAGTGT  
GACGCTCCCCGCCGCGTCCCACGCCATCCCGCATCTGACCACCAGCGAAATG  
GATTTTTGCATCGAGCTGGGTAATAAGCGTTGGCAATTTAACCGCCAGTCAG  
GCTTTCCTTTCACAGATGTGGATTGGCGATAAAAAACAACTGCTGACGCCGCT  
GCGCGATCAGTTCACCCGTGCACCGCTGGATAACGACATTGGCGTAAGTGAA  
GCGACCCGCATTGACCCTAACGCCTGGGTGCAACGCTGGAAGGCGGCGGGCC  
ATTACCAGGCCGAAGCAGCGTTGTTGCAGTGCACGGCAGATACACTTGCTGA  
TGCGGTGCTGATTACGACCGCTCACGCGTGGCAGCATCAGGGGAAAACCTTA  
TTTATCAGCCGGAAAACCTACCGGATTGATGGTAGTGGTCAAATGGCGATTA  
CCGTTGATGTTGAAGTGGCGAGCGATACACCGCATCCGGCGCGGATTGGCCT  
GAACTGCCAGCTGGCGCAGGTAGCAGAGCGGGTAAACTGGCTCGGATTAGG  
GCCGCAAGAAAACCTATCCCGACCGCCTTACTGCCGCCTGTTTTGACCGCTGGG  
ATCTGCCATTGTGACAGATGTATACTGGCTGCACCATCTGTCTTCATCTTCCC  
GCCATCTGATGAGCAGTTGAAATCTGAACTGCCTCTGTTGTGTGCCTGCTGA  
ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCT  
CCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAG  
CACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAA  
CACAAAGTATATGCCTGCGAAGTCACCCATCAGGGCCTGAGCTTGCCCGTCA  
CAAAGAGCTTCAACAGGGGAGAGTGTTAGTTCTAGATAATTAATTAGGAGGA  
ATTTAAAATGAAATACCTATTGCCTACGGCAGCCGCTGGATTGTTATTACTCG  
CTGCCCAACCAGCCATGGCCCTCGAGCTGATGAGCCATGGAAGCTGTGTGCG  
CTGCACCAGGCTCCACGGCTCGTGGTGCGGTGCGCTTCTGGTGTTGCTGCC  
TACAGCCGACACGTCGAGCTTCGTGCCCTAGAGTTGCGCGTCACAGCAGCC  
TCCGGCGCTCCGCGATATCACCGTGTCTATCCACATCAATGAAGTAGTGCTCCT  
AGACGCCCCCGTGGGGCTGGTGGCGCGGTTGGCTGACGAGAGCGGCCACGTA  
GTGTTGCGCTGGCTCCCGCCGCCTGAGACACCCATGACGTCTCACATCCGCTA  
CGAGGTGGACGTCTCGGCCGGCAACGGCGCAGGGAGCGTACAGAGGGTGA

Fig. 3B

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GATCCTGGAGGGCCGCACCGAGTGTGTGCTGAGCAACCTGCGGGGCCGGACG  
CGCTACACCTTCGCCGTCCGCGCGCGTATGGCTGAGCCGAGCTTCGGCGGCTT  
CTGGAGCGCCTGGTCGGAGCCTGTGTGCTGCTGACGCCTAGCGACCTGGAC  
CCCCTCATCCTGACGCTCTCCCTCATCCTCGTGGTCATCCTGGTGCTGCTGAC  
CGTGCTCGCGCTGCTCTCCCACCGCCGGGCTCTGAAGCAGAAGATCTGGCCT  
GGCATCCCCGAGCCCAGAGAGCGAGTTTGAAGGCCTCTTCACCACCCACAAGG  
GTAACCTCCAGCTGTGGCTGTACCAGAATGATGGCTGCCTGTGGTGGAGCCC  
CTGCACCCCTTCACGGAGGACCCACCTGCTTCCCTGGAAGTCCTCTCAGAGC  
GCTGCTGGGGGACGATGCAGGCAGTGGAGCCGGGGACAGATGATGAGGGCC  
CATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGC  
GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTGCG  
TGGAACCTCAGGCGCCCTGACCAGCGCGTGACACCTTCCCGGCTGTCTAC  
AGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAG  
CTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC  
AAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAAGTAGTGCCAG  
GCCGGCCAGCACCATCACCATGCGGCATACCCGTACGACGTTCCGG  
ACTACGCTTCTTAGGAGGGTGGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGG  
CGGCTCTGAGGGAGGCGGTTCCGGTGGTGGCTCTGGTTCCGGTGATTTTGATT  
ATGAAAAGATGGCAAACGCTAATAAGGGGGCTATGACCGAAAATGCCGATG  
AAAACGCGCTACAGTCTGACGCTAAAGGCAAACCTTGATTCTGTGCTACTGA  
TTACGGTGCTGCTATCGATGGTTTCATTGGTGACGTTTCCGGCCTTGCTAATG  
GTAATGGTGCTACTGGTGATTTTGCTGGCTCTAATTCCCAAATGGCTCAAGTC  
GGTGACGGTGATAATTCACCTTTAATGAATAATTTCCGTCAATATTTACCTTC  
CCTCCCTCAATCGGTTGAATGTCGCCCTTTTGTCTTTAGCGCTGGTAAACCAT  
ATGAATTTTCTATTGATTGTGACAAAATAAACTTATTCCGTGGTGTCTTTGCG  
TTTCTTTTATATGTTGCCACCTTTATGTATGTATTTTCTACGTTTGCTAACATA  
CTGCGTAATAAGGAGTCTTAAGCTAGCTAATTAATTTAAGCGGCCGCAGATC  
T3'

Fig. 3C

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(SEQ. ID No. 1)

Ssp I  
|

GGGAAATTGTAAGCGTTAATATTTTGTAAATTCGCGTTAAATTTTGTAAATCAGC  
 ....|....|....|....|....|....|....|....|....|....|....|.... 59

Psi I  
|

TCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGAC  
 |....|....|....|....|....|....|....|....|....|....|....|.... 118

CGAGATAGGGTTGAGTGTGTTCCAGTTTGAACAAGAGTCCACTATTAAAGAACGTGG  
 .|....|....|....|....|....|....|....|....|....|....|....|... 177

Drd I  
|

Ade I  
Dra III  
|

ACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCA  
 ..|....|....|....|....|....|....|....|....|....|....|....|. 236

TCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAA  
 ...|....|....|....|....|....|....|....|....|....|....|....|.... 295

NgoM IV  
|

Nae I  
|

AGGGAGCCCCCGATTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAG  
 ....|....|....|....|....|....|....|....|....|....|....|....|.... 354

BsrB I  
Mbi I  
|

GGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGC  
 |....|....|....|....|....|....|....|....|....|....|....|.... 413

Fig. 4A

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GTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTT  
 . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . 472

TCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTCTAAATACATTCAAATATGT  
 .. | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . 531

BsrB I  
 Mbi I  
 BspH I  
 Bci VI  
 Ssp I  
 Ear I  
 ATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGT  
 . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . 590

ATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCTTCC  
 . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . 649

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Amp frag

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Alw44 I  
 ApaL I  
 TGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGGTG  
 | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . 708

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Amp frag

---

BssS I  
 Eco57 I  
 CACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGC  
 . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . 767

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Amp frag

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Fig. 4B

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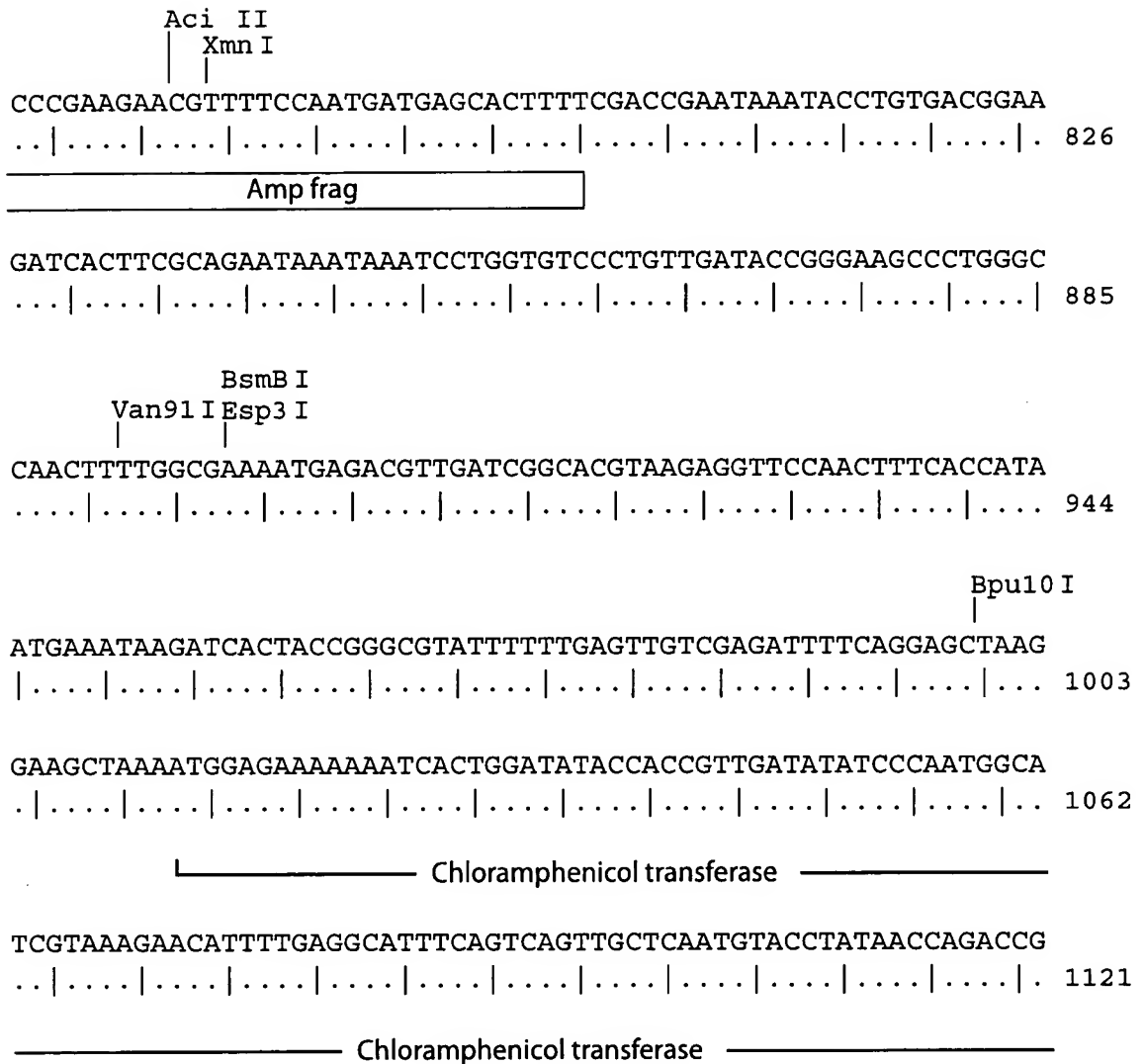


Fig.4C



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Pvu II                      Dra I  
 |                              |  
 TTCAGCTGGATATTACGGCCTTTTAAAGACCGTAAAGAAAAATAAGCACAAGTTTAT  
 ...|...|...|...|...|...|...|...|...|...|...|...| 1180

————— Chloramphenicol transferase —————

BsaMI                      Acc III                      SnaBI  
 |                              |                              |  
 CCGGCCTTTATTACATTCTTGCCCGCTGATGAATGCTCATCCGGAATTACGTATGGC  
 ....|...|...|...|...|...|...|...|...|...|...|...| 1239

————— Chloramphenicol transferase —————

BseMI                      BsrDI  
 |                              |  
 AATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTTACCCTTGTTACACCGTTTCC  
 |...|...|...|...|...|...|...|...|...|...|...|...| 1298

————— Chloramphenicol transferase —————

Aci II    BpmI  
 |    |  
 ATGAGCAAACGTTTTCATCGCTCTGGAGTGAATACCACGACGATTTCCGGCAG  
 .|...|...|...|...|...|...|...|...|...|...|...|.. 1357

————— Chloramphenicol transferase —————

TTTCTACACATATATTCGCAAGATGTGGCGTGTTACGGTGAAAACCTGGCCTATTTCCC  
 ..|...|...|...|...|...|...|...|...|...|...|...|. 1416

————— Chloramphenicol transferase —————

Fig. 4D

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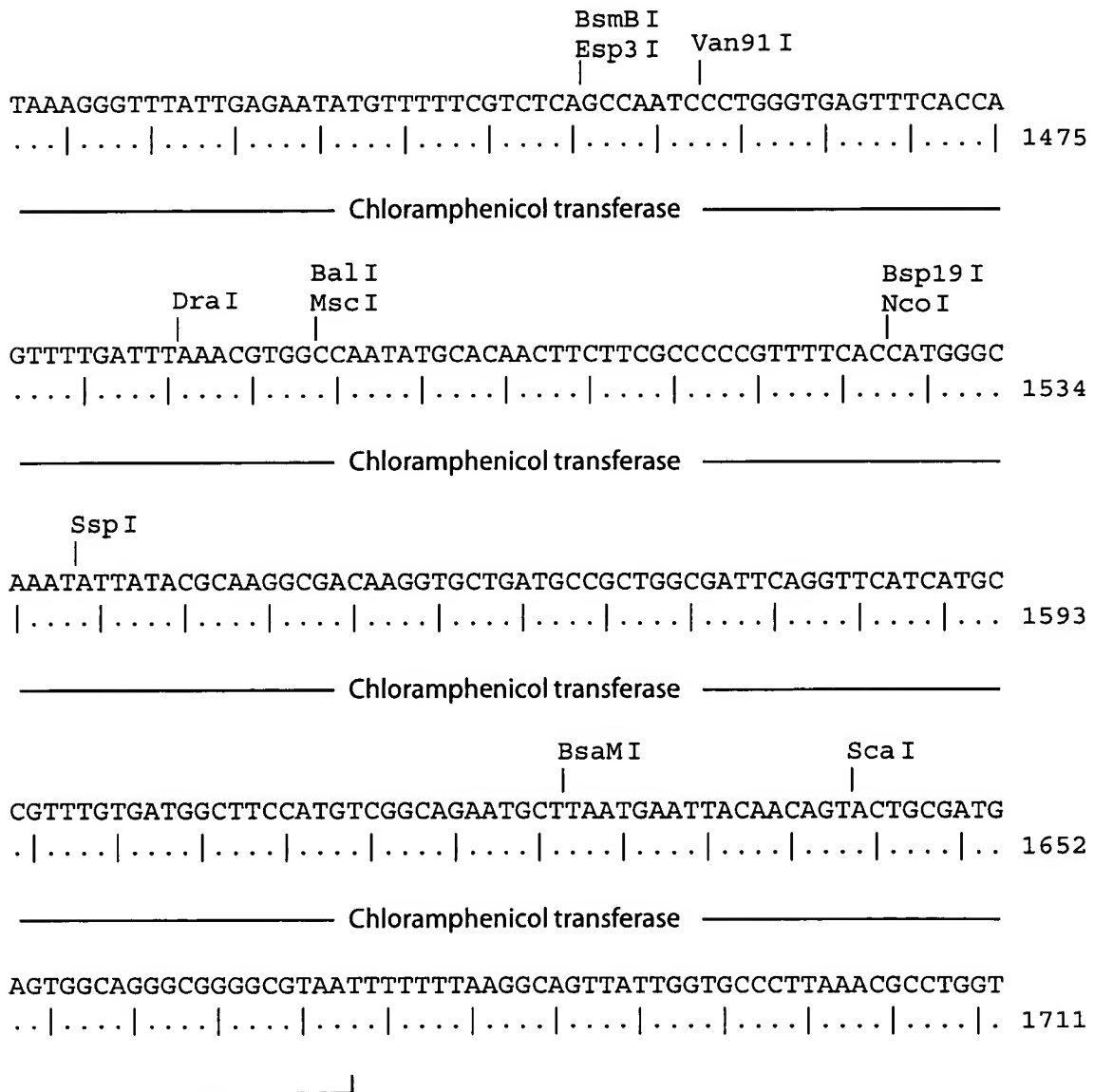


Fig.4E

REPLACEMENT SHEET

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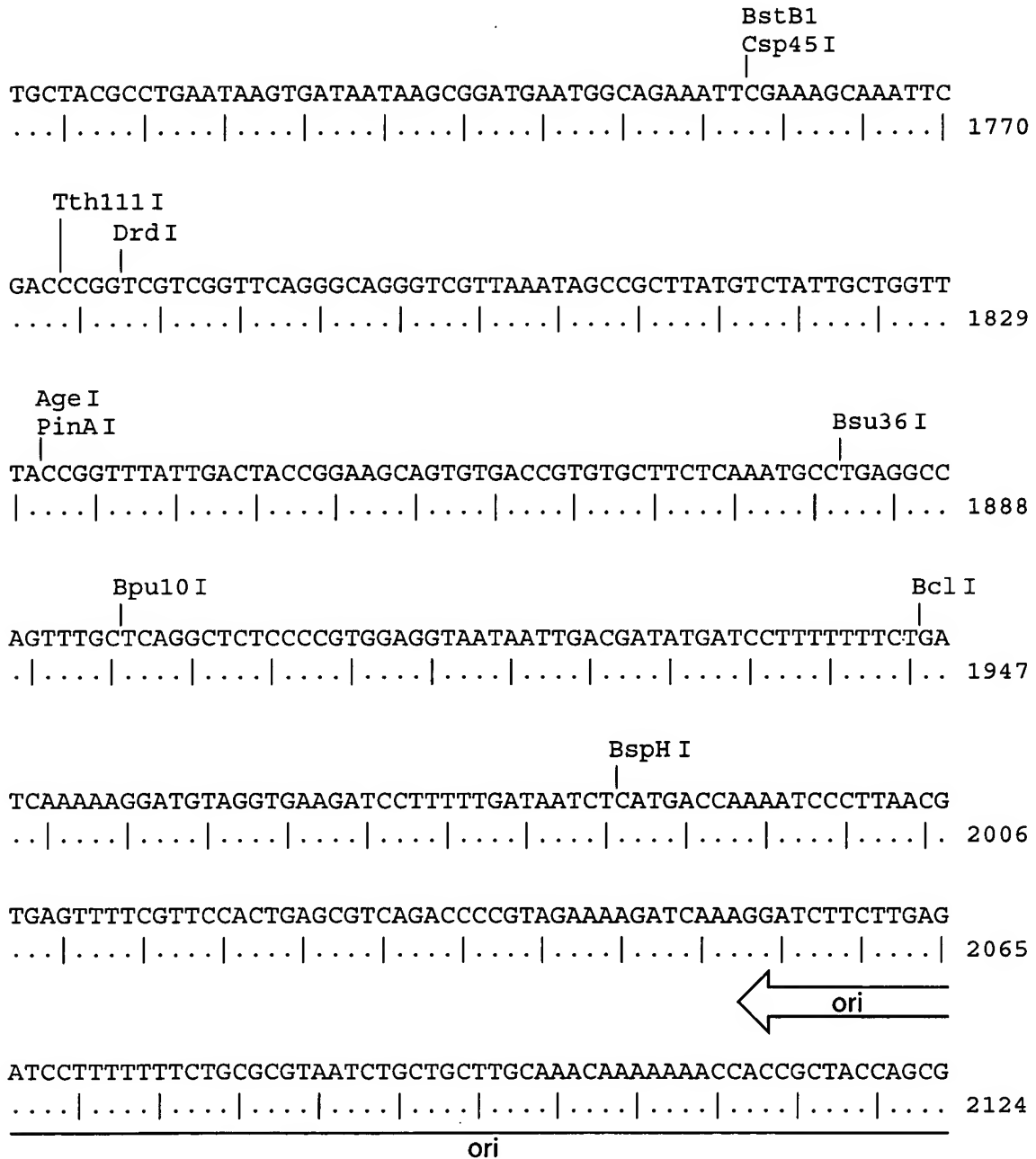


Fig. 4F

# REPLACEMENT SHEET

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		Eco57 I	
GTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTCCGAAGGTAAGTGGCTTCAG			
... ... ... ... ... ... ... ... ... ... ... ... ...	2183		
<hr/>			
ori			
<hr/>			
CAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCA			
. ... ... ... ... ... ... ... ... ... ... ... ... ..	2242		
<hr/>			
ori			
<hr/>			
		AlwNI	
AGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCT			
.. ... ... ... ... ... ... ... ... ... ... ... ..	2301		
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ori			
<hr/>			
GCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAA			
... ... ... ... ... ... ... ... ... ... ... ... ...	2360		
<hr/>			
ori			
<hr/>			
		Alw44 I	
		ApaLI	
GGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGA			
.... ... ... ... ... ... ... ... ... ... ... ... ....	2419		
<hr/>			
ori			
<hr/>			
CCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAA			
... ... ... ... ... ... ... ... ... ... ... ... ...	2478		
<hr/>			
ori			
<hr/>			

Fig. 4G

**Fig. 4H**

# REPLACEMENT SHEET

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Fig. 4l



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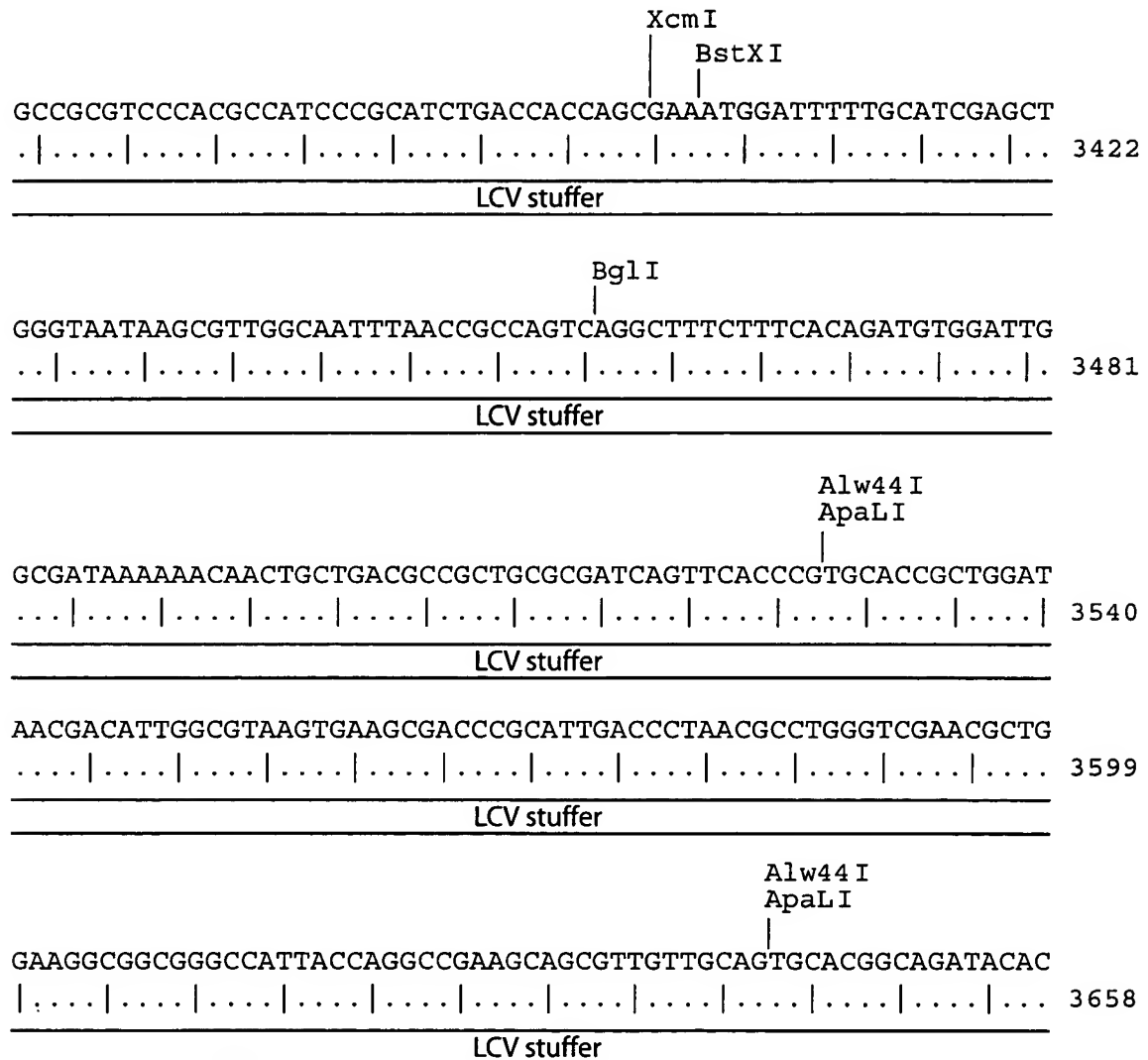


Fig. 4K



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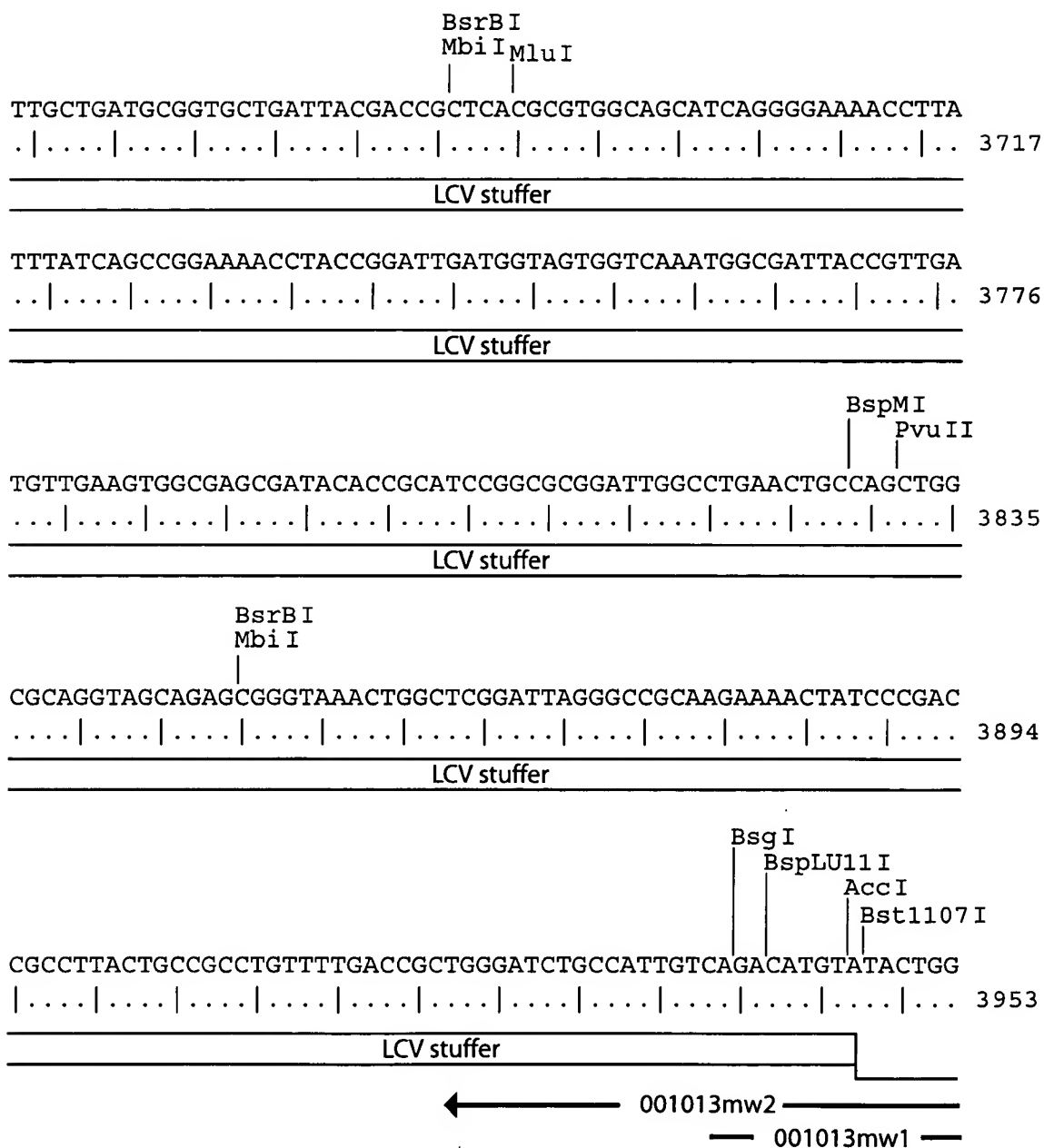


Fig. 4L

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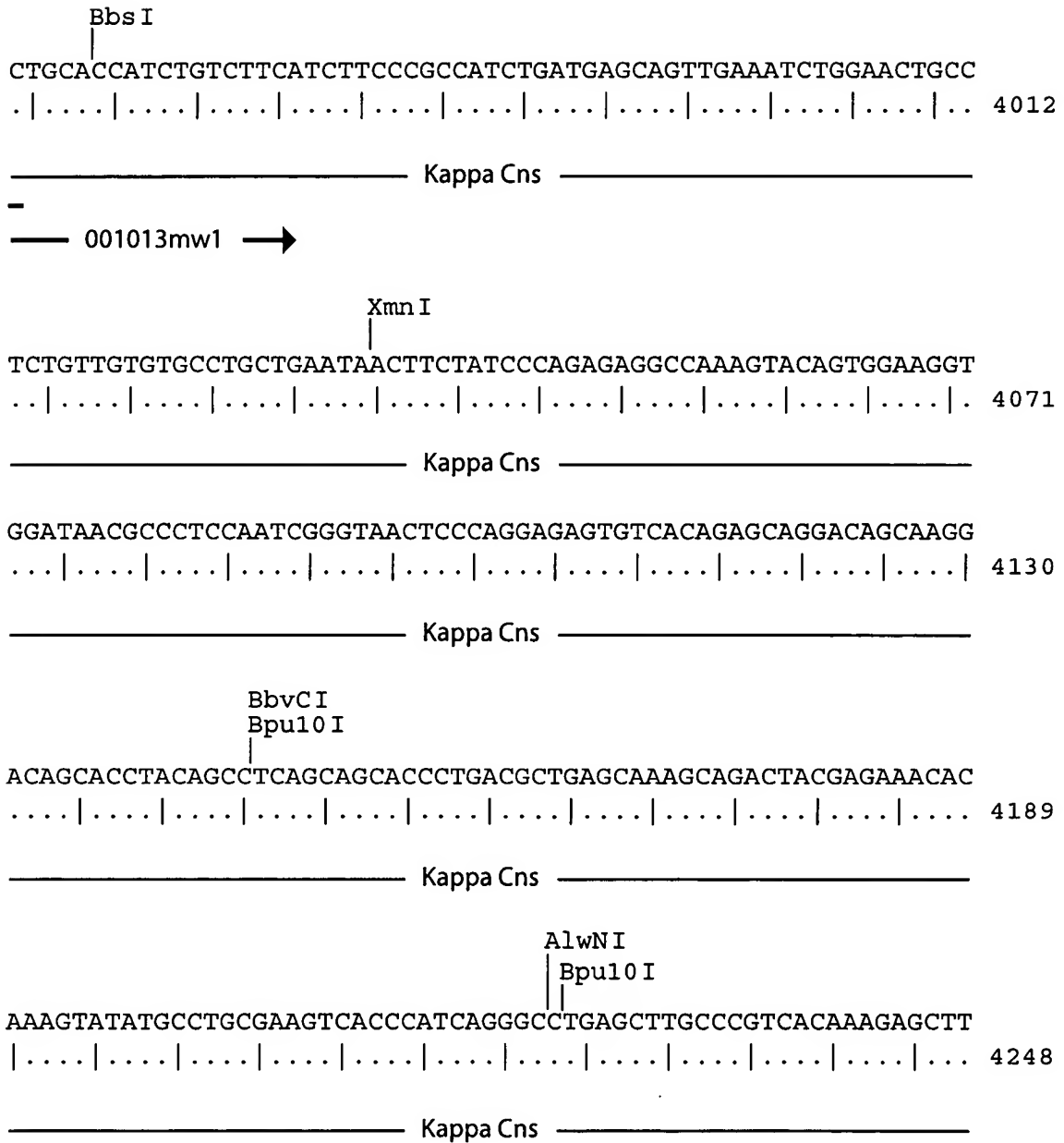


Fig. 4M

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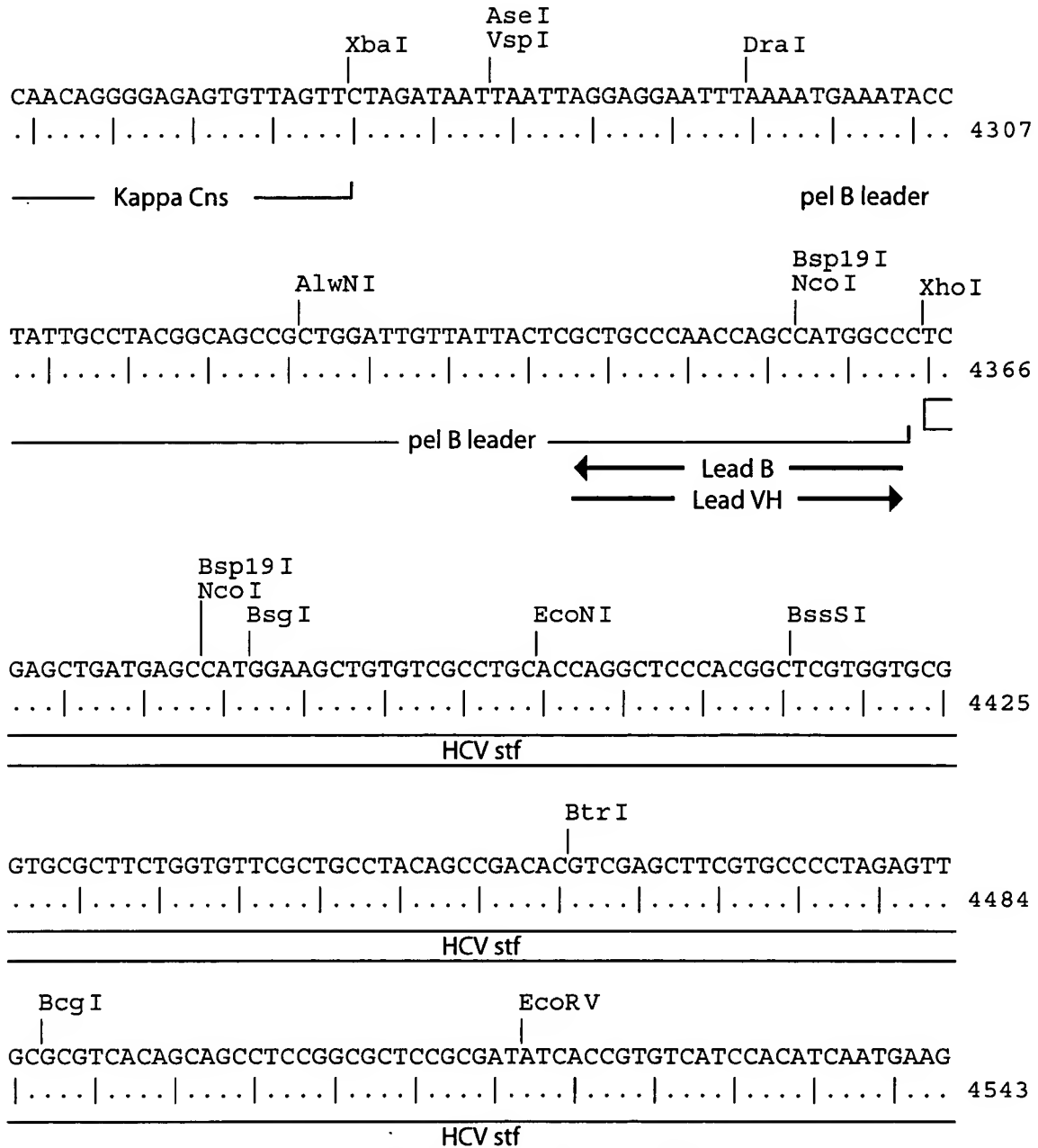


Fig. 4N

Fig. 40



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Bcu I  
 Bcu I    Bal I  
 Spe I    Msc I
 
  
 CCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAAGTAGTGGC
 5487

Fig. 4Q

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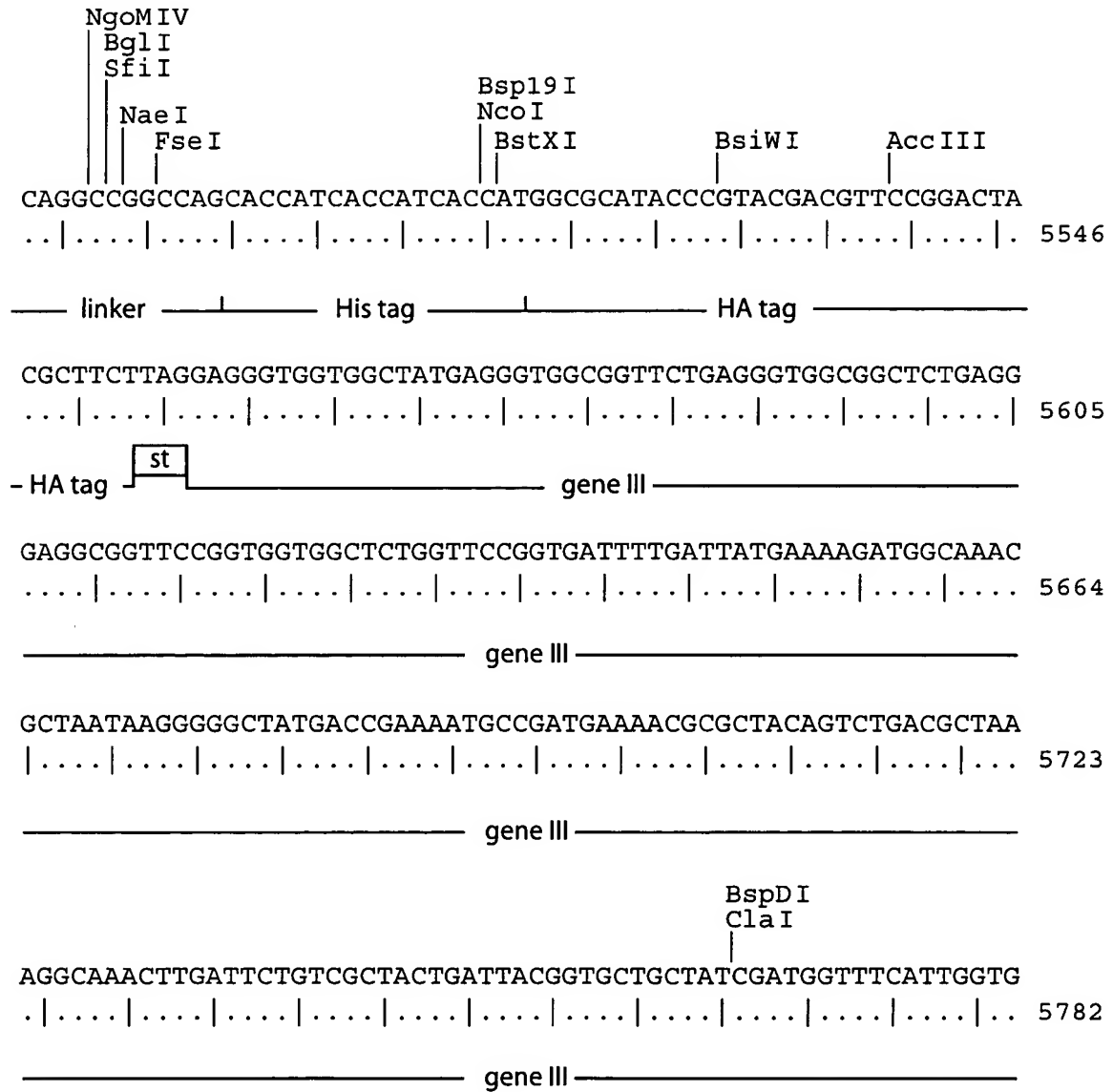


Fig.4R

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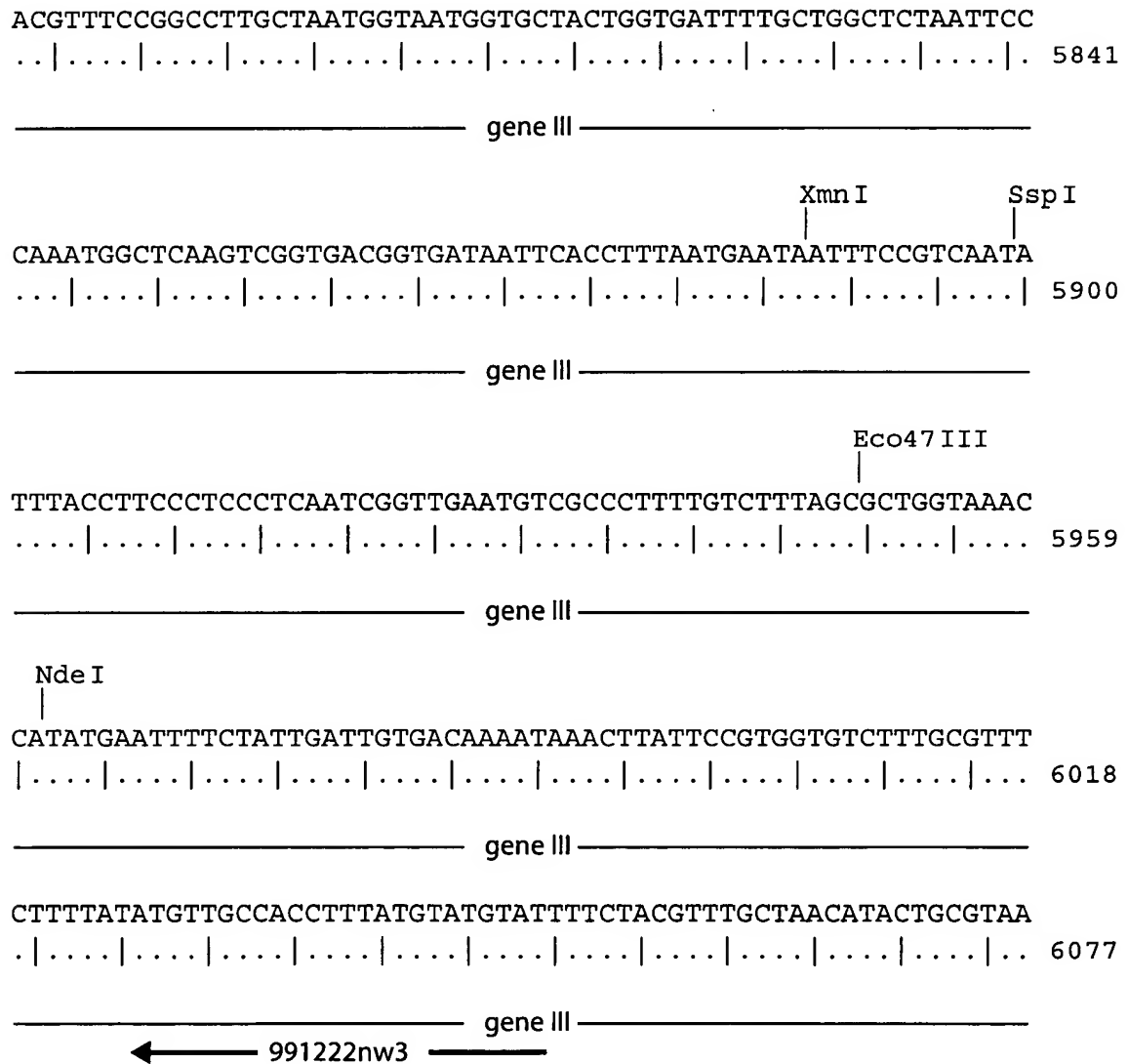


Fig. 4S



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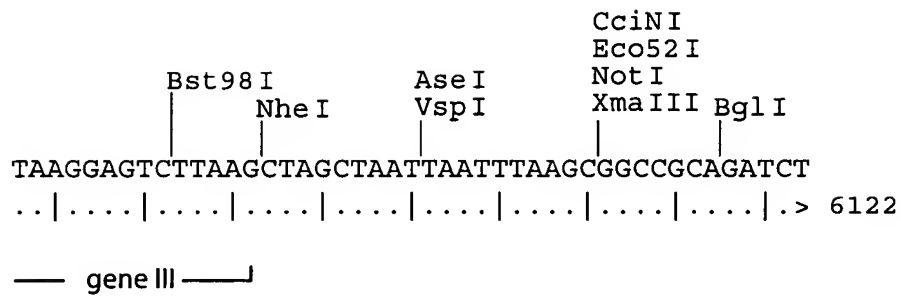


Fig.4T

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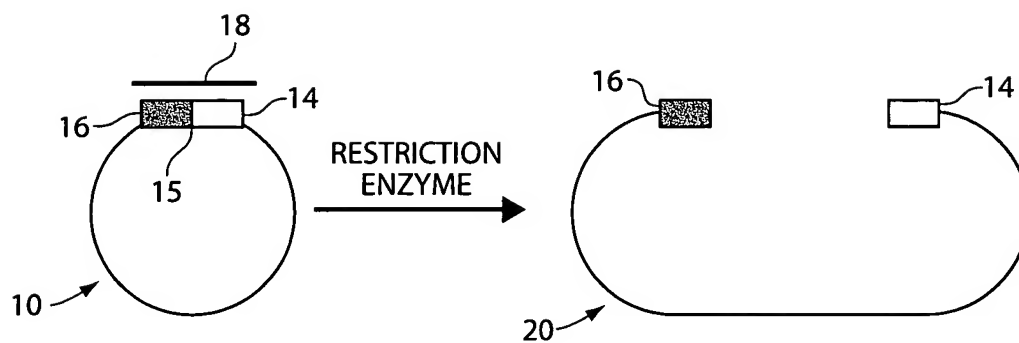


Fig. 5A

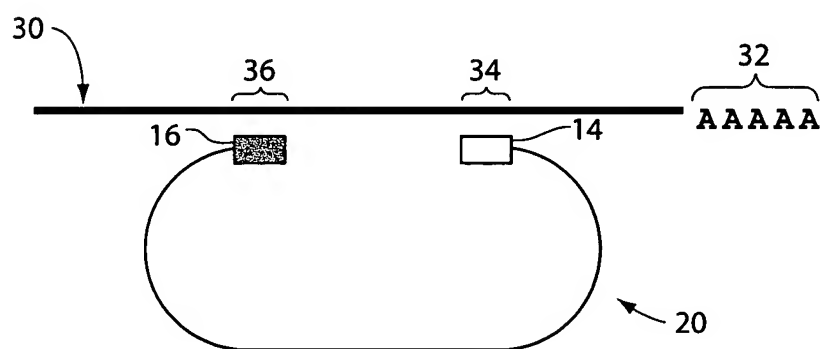


Fig. 5B

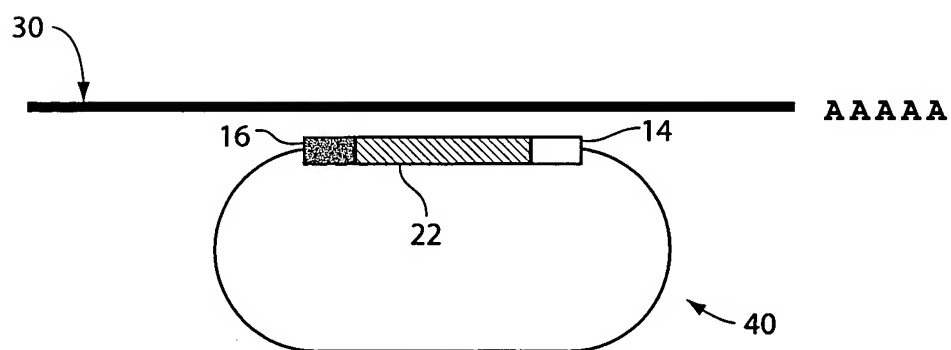


Fig. 5C

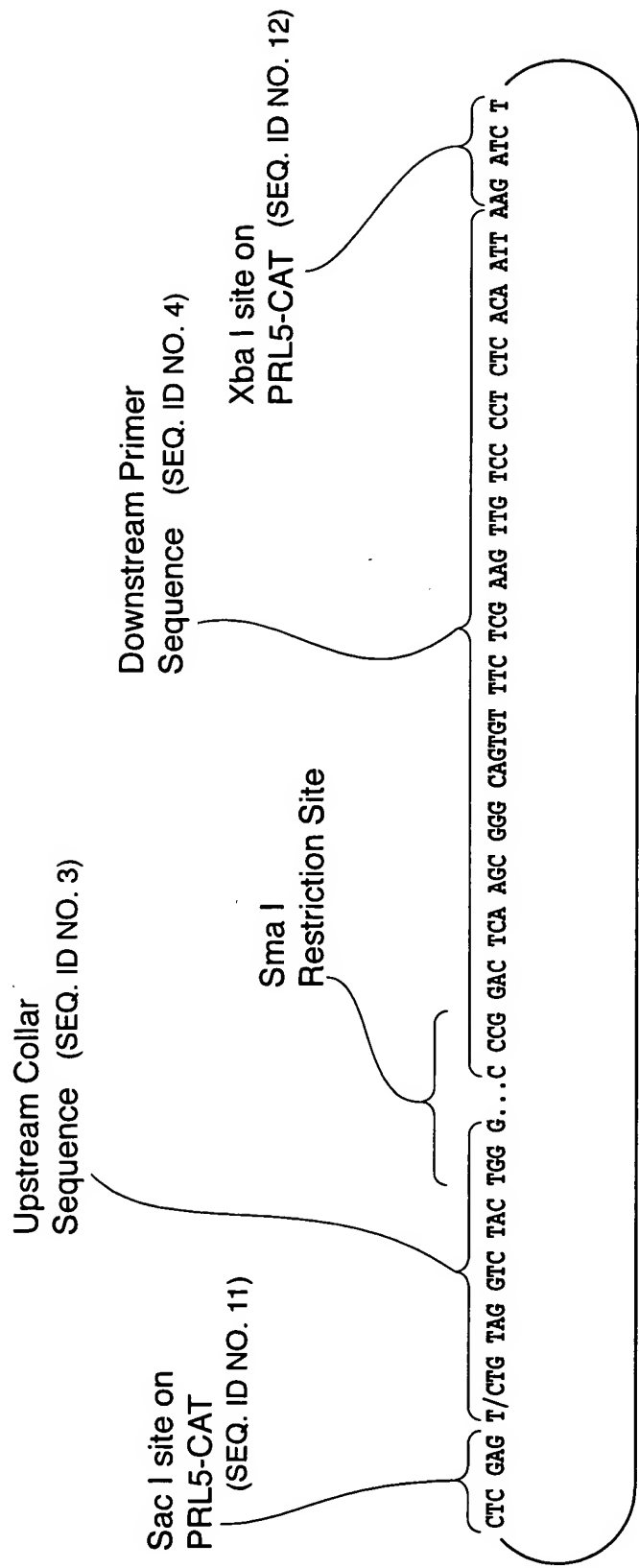


Fig. 6A

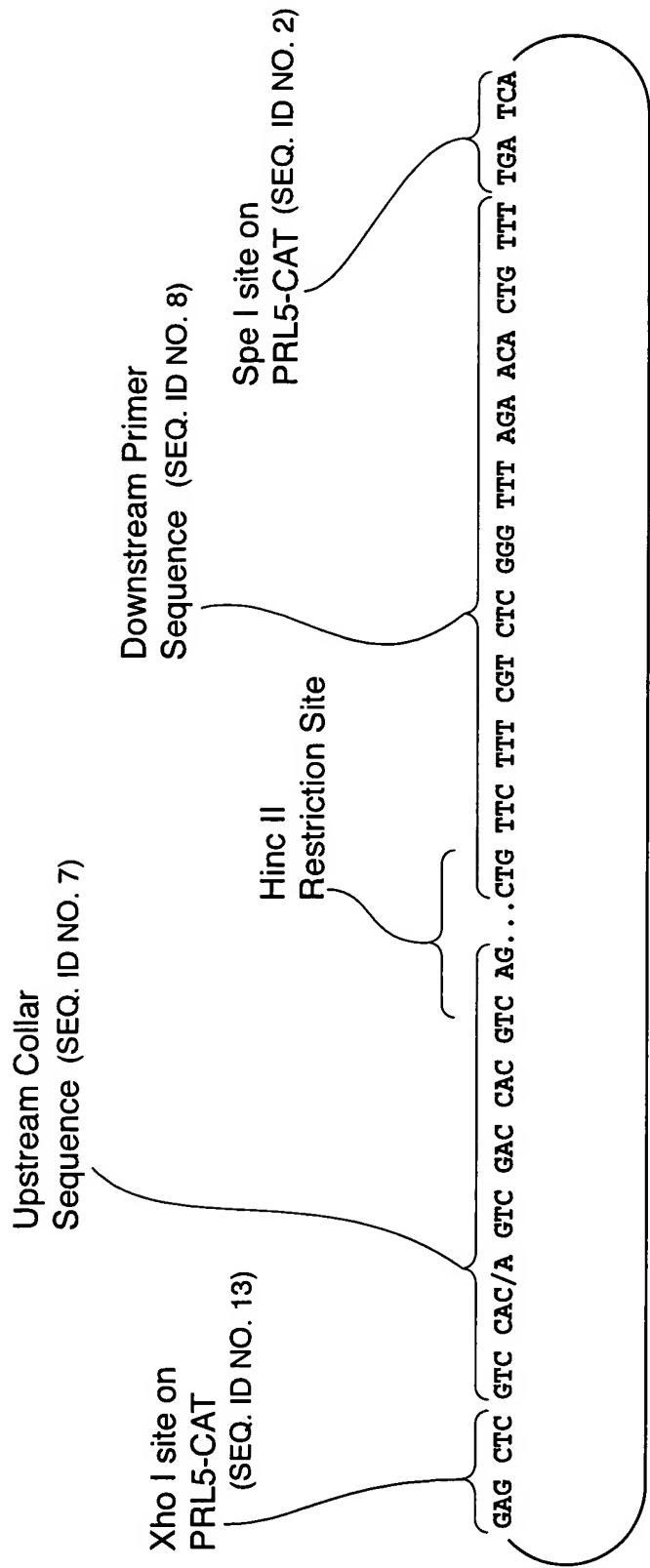


Fig.6B

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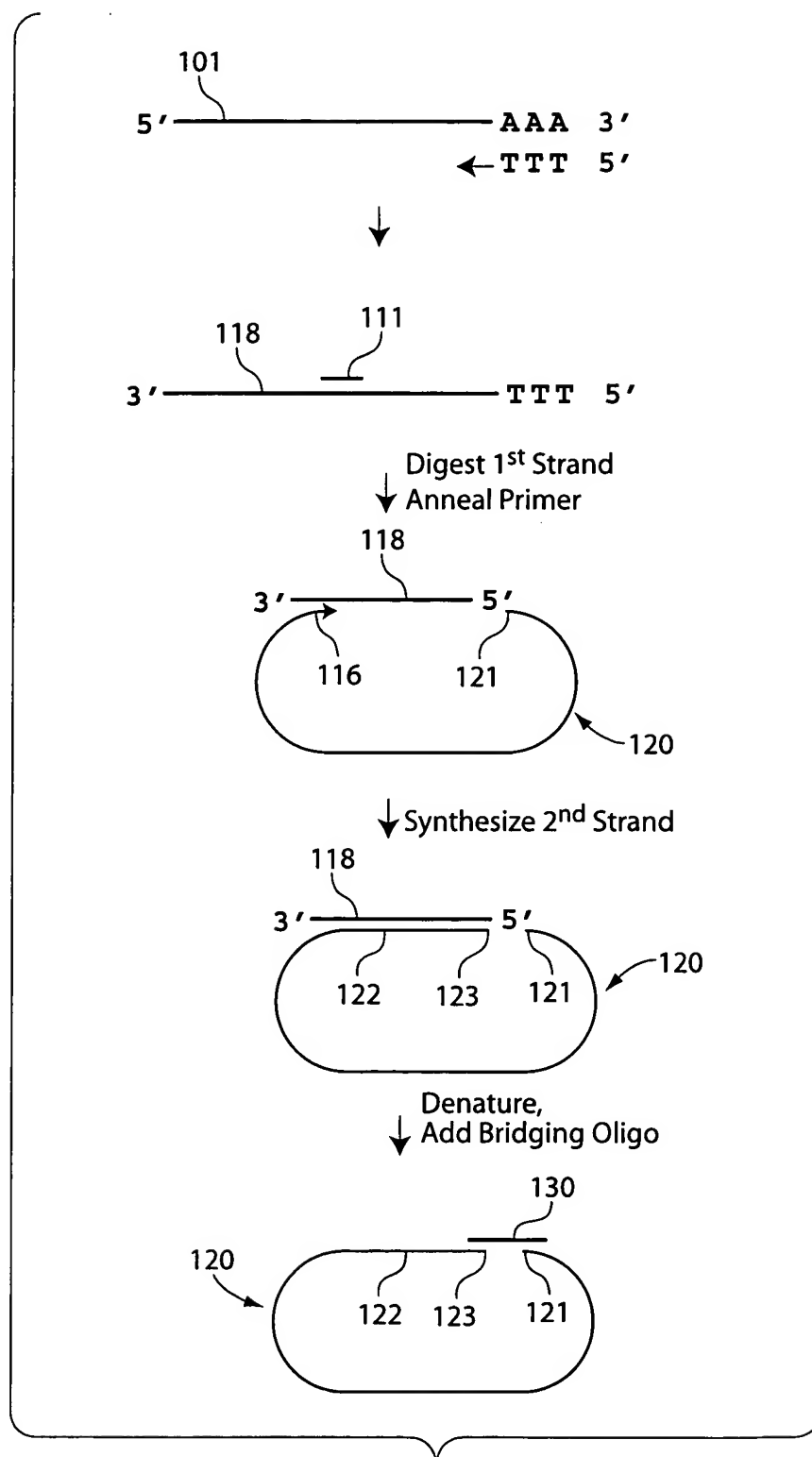


Fig. 7